

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/571,836  
Source: IFWP  
Date Processed by STIC: 12/29/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 12/29/2006

PATENT APPLICATION: US/10/571,836

TIME: 15:35:31

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\12292006\J571836.raw

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3 <110> APPLICANT: Jialin, Sun
5 <120> TITLE OF INVENTION: A superantigen fusion protein for anti-cancer therapy and
methods for the
6     production thereof
8 <130> FILE REFERENCE: 09548.1019USWO
10 <140> CURRENT APPLICATION NUMBER: 10/571,836
11 <141> CURRENT FILING DATE: 2006-03-15
13 <150> PRIOR APPLICATION NUMBER: PCT/CN2004/000569
14 <151> PRIOR FILING DATE: 2004-05-31
16 <150> PRIOR APPLICATION NUMBER: CN 200310109829.7
17 <151> PRIOR FILING DATE: 2003-12-21
19 <160> NUMBER OF SEQ ID NOS: 15
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 903
25 <212> TYPE: DNA
26 <213> ORGANISM: artificial sequence
28 <220> FEATURE:
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (1)..(903)
31 <223> OTHER INFORMATION: coding sequence of fusion protein
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35 atgtatatgt aggcctaga caagtacgcg tgtaattgcg ttgttggcta catcgggtgag      120
36 cgctgtcagt atcgagatct gaaatggtgg gaacttagag gtggaggcgg ttcaggcgga      180
37 ggtggctctg gcggtggcgg atcgagcgag aaaagcgaag aaataaatga aaaagatttg      240
38 cgaaaaaagt ctgaattgca gggaacagct ttaggcaatc ttaaacaat ctattattac      300
39 aatgaaaaag ctaaaactga aaataaagag agtcacgata aattttttaca gcatactata      360
40 ttgttttaag gcttttttac agatcattcg tgggtataacg atttattagt agattttgat      420
41 tcaaaggata ttgttgataa atataaaggg aaaaaagtag acttgtagtg tgcttattat      480
42 ggttatcaat gtgcgggtgg tacaccaaac aaaacagctt gtatgtatgg tgggtgtaacg      540
43 ttacatgata ataatcgatt gaccgaagag aaaaaagtgc cgatcaattt atggctagac      600
44 ggtaaacaaa atacagtacc tttggaaacg gttaaaacga ataagaaaaa tgtaactggt      660
45 caggagttgg atcttcaagc aagacgttat ttacaggaaa aatataattt atataactct      720
46 gatgtttttg atgggaaggt tcagaggggga ttaatcgtgt ttcatacttc tacagaacct      780
47 tcggttaatt acgattttatt tgggtgctcaa ggacagtatt caaatacact attaagaata      840
48 tatagagata ataaaacgat taactctgaa aacatgcata ttgatataata tttatataca      900
49 agt
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 301
53 <212> TYPE: PRT
54 <213> ORGANISM: artificial sequence
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature

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58 <222> LOCATION: (1)..(301)
59 <223> OTHER INFORMATION: fusion protein
67 <400> SEQUENCE: 2
68 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
69 1 5 10 15
70 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
71 20 25 30
72 Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
73 35 40 45
74 Trp Trp Glu Leu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
75 50 55 60
76 Gly Gly Gly Ser Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu
77 65 70 75 80
78 Arg Lys Lys Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln
79 85 90 95
80 Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His
81 100 105 110
82 Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp
83 115 120 125
84 His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile
85 130 135 140
86 Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr
87 145 150 155 160
88 Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr
89 165 170 175
90 Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys
91 180 185 190
92 Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu
93 195 200 205
94 Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp
95 210 215 220
96 Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser
97 225 230 235 240
98 Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr
99 245 250 255
100 Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln
101 260 265 270
102 Tyr Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn
103 275 280 285
104 Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr Ser
105 290 295 300
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 1107
109 <212> TYPE: DNA
110 <213> ORGANISM: artificial sequence
112 <220> FEATURE:
113 <221> NAME/KEY: misc_feature
114 <222> LOCATION: (1)..(1107)
115 <223> OTHER INFORMATION: coding sequence of fusion protein

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117 <400> SEQUENCE: 3
118 gcacccatgg cagaaggagg agggcagaat catcacgaag tggatgaagtt catggatgtc      60
119 tatcagcgca gctactgcca tccaatcgag accctggtgg acatcttcca ggagtaccct      120
120 gatgagatcg agtacatctt caagccatcc tgtgtgcccc tgatgcgatg cgggggctgc      180
121 tgcaatgacg agggcctgga gtgtgtgccc actgaggagt ccaacatcac catgcagatt      240
122 atgcggtatca aacctcacca aggccagcac ataggagaga tgagcttcct acagcacaac      300
123 aaatgtgaat gcagaccaa gaaagataga gcaagacaag aaaaatgtga caagccgagg      360
124 cgggggtggag gcggttcagg cggaggtggc tctggcgggtg gcggatcgag cgagaaaagc      420
125 gaagaaataa atgaaaaaga tttgcaaaaa aagtctgaat tgcaggggaa agctttaggc      480
126 aatcttaaac aaatctatta ttacaatgaa aaagctaaaa ctgaaaataa agagagtcac      540
127 gatcaatttt tacagcatat tatattgttt aaaggctttt ttacagatca ttcgtggtat      600
128 aacgatttat tagtagattt tgattcaaag gatattgttg ataaatataa agggaaaaaa      660
129 gtagacttgt atggtgctta ttatggttat caatgtgcgg gtggtacacc aaacaaaaca      720
130 gcttgtatgt atggtggtgt aacgttacat gataataatc gattgaccga agagaaaaaa      780
131 gtgccgatca atttatggct agacggtaaa caaaatacag tacctttgga aacggttaaa      840
132 acgaataaga aaaatgtaac tgttcaggag ttggatcttc aagcaagacg ttatttacag      900
133 gaaaaatata atttatataa ctctgatggt tttgatggga aggttcagag gggattaatc      960
134 gtgtttcata cttctacaga accttcgggt aattacgatt tatttggtgc tcaaggacag      1020
135 tattcaaata cactattaag aatatataga gataataaaa cgattaactc tgaaaacatg      1080
136 catattgata tatatttata tacaagt      1107
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 369
140 <212> TYPE: PRT
141 <213> ORGANISM: artificial sequence
143 <220> FEATURE:
144 <221> NAME/KEY: misc_feature
145 <222> LOCATION: (1)..(369)
146 <223> OTHER INFORMATION: fusion protein
148 <400> SEQUENCE: 4
149 Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys
150 1 5 10 15
151 Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu
152 20 25 30
153 Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys
154 35 40 45
155 Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
156 50 55 60
157 Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile
158 65 70 75 80
159 Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe
160 85 90 95
161 Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg
162 100 105 110
163 Gln Glu Lys Cys Asp Lys Pro Arg Gly Gly Gly Gly Ser Gly Gly
164 115 120 125
165 Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Lys Ser Glu Glu Ile Asn
166 130 135 140
167 Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Thr Ala Leu Gly
168 145 150 155 160

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169 Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
170                               165                               170                               175
171 Lys Glu Ser His Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly
172                               180                               185                               190
173 Phe Phe Thr Asp His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp
174                               195                               200                               205
175 Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr
176                               210                               215                               220
177 Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr
178 225                               230                               235                               240
179 Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr
180                               245                               250                               255
181 Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
182                               260                               265                               270
183 Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val
184                               275                               280                               285
185 Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn
186                               290                               295                               300
187 Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile
188 305                               310                               315                               320
189 Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
190                               325                               330                               335
191 Ala Gln Gly Gln Tyr Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn
192                               340                               345                               350
193 Lys Thr Ile Asn Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr
194                               355                               360                               365
195 Ser

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198 &lt;210&gt; SEQ ID NO: 5

199 &lt;211&gt; LENGTH: 45

200 &lt;212&gt; TYPE: DNA

201 &lt;213&gt; ORGANISM: artificial sequence

203 &lt;220&gt; FEATURE:

204 &lt;221&gt; NAME/KEY: misc\_feature

205 &lt;222&gt; LOCATION: (1)..(45)

206 &lt;223&gt; OTHER INFORMATION: primer

208 &lt;400&gt; SEQUENCE: 5

209 ggtggaggcg gtccagggcg aggtggctct ggcggtggcg gatcg

45

211 &lt;210&gt; SEQ ID NO: 6

212 &lt;211&gt; LENGTH: 15

213 &lt;212&gt; TYPE: PRT

214 &lt;213&gt; ORGANISM: artificial sequence

216 &lt;220&gt; FEATURE:

217 &lt;221&gt; NAME/KEY: misc\_feature

218 &lt;222&gt; LOCATION: (1)..(15)

219 &lt;223&gt; OTHER INFORMATION: linker peptide

221 &lt;400&gt; SEQUENCE: 6

223 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

224 1 5 10 15

226 &lt;210&gt; SEQ ID NO: 7

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Input Set : A:\PTO.SS.txt

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227 <211> LENGTH: 34
228 <212> TYPE: DNA
229 <213> ORGANISM: artificial sequence
231 <220> FEATURE:
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (1)..(34)
234 <223> OTHER INFORMATION: primer
236 <400> SEQUENCE: 7
237 gagccccgggc agcgagaaaa gcgaagaaat aaat 34
239 <210> SEQ ID NO: 8
240 <211> LENGTH: 40
241 <212> TYPE: DNA
242 <213> ORGANISM: artificial sequence
244 <220> FEATURE:
245 <221> NAME/KEY: misc_feature
246 <222> LOCATION: (1)..(40)
247 <223> OTHER INFORMATION: primer
249 <400> SEQUENCE: 8
250 gtgcggccgc acttgatat aaatatatat caatatgcat 40
252 <210> SEQ ID NO: 9
253 <211> LENGTH: 28
254 <212> TYPE: DNA
255 <213> ORGANISM: artificial sequence
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (1)..(28)
260 <223> OTHER INFORMATION: primer
262 <400> SEQUENCE: 9
263 gagccccgggc aattccgata gcgagtgt 28
265 <210> SEQ ID NO: 10
266 <211> LENGTH: 28
267 <212> TYPE: DNA
268 <213> ORGANISM: artificial sequence
270 <220> FEATURE:
271 <221> NAME/KEY: misc_feature
272 <222> LOCATION: (1)..(28)
273 <223> OTHER INFORMATION: primer
275 <400> SEQUENCE: 10
276 gtgcggccgc tctaagttcc caccattt 28
278 <210> SEQ ID NO: 11
279 <211> LENGTH: 31
280 <212> TYPE: DNA
281 <213> ORGANISM: artificial sequence
283 <220> FEATURE:
284 <221> NAME/KEY: misc_feature
285 <222> LOCATION: (1)..(31)
286 <223> OTHER INFORMATION: primer
288 <400> SEQUENCE: 11
289 gagccccgggc gcacccatgg cagaaggagg a 31

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\PTO.SS.txt  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/571,836**

DATE: 12/29/2006

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Input Set : **A:\PTO.SS.txt**

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